RAW SEQUENCE LISTING

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Application Serial Number: 10/006,305A
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RAW SEQUENCE LISTING DATE: 10/29/2004
PATENT APPLICATION: **US/10/006,305A** TIME: 13:08:30

Input Set : **A:\41673292.app**
Output Set: **N:\CRF4\10292004\J006305A.raw**

<110> APPLICANT: PRUSSAK, CHARLES E.
KIPPS, THOMAS J.
CANTWELL, MARK J.
<120> TITLE OF INVENTION: NOVEL CHIMERIC TNF LIGANDS
<130> FILE REFERENCE: 041673-2092
<140> CURRENT APPLICATION NUMBER: 10/006,305A
<141> CURRENT FILING DATE: 2001-12-06
<160> NUMBER OF SEQ ID NOS: 8
<170> SOFTWARE: PatentIn Ver. 3.2
<210> SEQ ID NO: 1
<211> LENGTH: 771
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct comprising Domain IV of hTNFa linked to Domains I, II, and III of hCD154
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atgaaaattt ttatgtattt acttactgtt tttcttatca cccagatgat tgggtcagca 120
ctttttgctg tgtatcttca tagaaggctg gacaagatag aagatgaaag gaatcttcat 180
gaagattttg tattcatgaa aacgatacag agatgcaaca caggagaaag atccttatcc 240
ttactgaact gtgaggagat taaaagccag tttgaaggct ttgtgaagga tataatgtta 300
aacaaagagg agacgaagaa agatgaggat cctgtagccc atgttgtagc aaaccctcaa 360
gctgaggggc agctccagtg gctgaaccgc cgggccaatg ccctcctggc caatggcgtg 420
gagctgagag ataaccagct ggtggtgcca tcagagggcc tgtacctcat ctactcccag 480
gtcctcttca agggccaagg ctgcccctcc acccatgtgc tcctcaccca caccatcagc 540
cgcatcgccg tctcctacca gaccaaggtc aacctcctct ctgccatcaa gagcccctgc 600
cagagggaga ccccagaggg ggctgaggcc aagccctggt atgagcccat ctatctggga 660
ggggtcttcc agctggagaa gggtgaccga ctcagcgctg agatcaatcg gcccgactat 720
ctcgactttg cggagtctgg gcaggtctac tttggaatca ttgctctgtg a 771
<210> SEQ ID NO: 2
<211> LENGTH: 580
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct comprising Domain IV of hTNFa linked to Domains I, II, and III of hCD70
<400> SEQUENCE: 2
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gctgctttgg tcccattggt cgcgggcttg gtgatctgcc tcgtggtgtg catccagcgc 120
ttcgcacagg ctgcggatcc tgtagcccat gttgtagcaa accctcaagc tgaggggcag 180

RAW SEQUENCE LISTING DATE: 10/29/2004
PATENT APPLICATION: **US/10/006,305A** TIME: 13:08:30

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Output Set: **N:\CRF4\10292004\J006305A.raw**

ctccagtggc tgaaccgccg ggccaatgcc ctcctggcca atggcgtgga gctgagagat 240
aaccagctgg tggtgccatc agagggcctg tacctcatct actcccaggt cctcttcaag 300
ggccaaggct gcccctccac ccatgtgctc ctcacccaca ccatcagccg catcgccgtc 360
tcctaccaga ccaaggtcaa cctcctctct gccatcaaga gcccctgcca gagggagacc 420
ccagaggggg ctgaggccaa gccctggtat gagcccatct atctgggagg ggtcttccag 480
ctggagaagg gtgaccgact cagcgctgag atcaatcggc ccgactatct cgactttgcg 540
gagtctgggc aggtctactt tggaatcatc gctctgtgaa 580

<210> SEQ ID NO: 3
<211> LENGTH: 837
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct comprising Domain IV of hTNFa linked to Domains I, II, III of hFasL

<400> SEQUENCE: 3
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tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
ggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaacca cagcacaggc 240
ctgtgtctcc ttgtgatgtt tttcatggtt ctggttgcct tggtaggatt gggcctgggg 300
atgtttcagc tcttccacct acagaaggag ctggcagaac tccgagagtc taccagccag 360
atgcacacag catcatcttt ggagaagcaa gcggatcctg tagcccatgt tgtagcaaac 420
cctcaagctg aggggcagct ccagtggctg aaccgccggg ccaatgccct cctggccaat 480
ggcgtggagc tgagagataa ccagctggtg gtgccatcag agggcctgta cctcatctac 540
tcccaggtcc tcttcaaggg ccaaggctgc ccctccaccc atgtgctcct cacccacacc 600
atcagccgca tcgccgtctc ctaccagacc aaggtcaacc tcctctctgc catcaagagc 660
ccctgccaga gggagacccc agaggggget gaggccaagc cctggtatga gcccatctat 720
ctgggagggg tcttccagct ggagaagggt gaccgactca gcgctgagat caatcggccc 780
gactatctcg actttgcgga gtctgggcag gtctactttg gaatcattgc tctgtga 837

<210> SEQ ID NO: 4
<211> LENGTH: 813
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct comprising Domain IV of hTNFa linked to Domains I, II, and III of hTRAIL

<400> SEQUENCE: 4
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atcttcacag tgctcctgca gtctctctgt gtggctgtaa cttacgtgta ctttaccaac 120
gagctgaagc agatgcagga caagtactcc aaaagtggca ttgcttgttt cttaaaagaa 180
gatgacagtt attgggaccc caatgacgaa gagagtatga acagcccctg ctggcaagtc 240
aagtggcaac tccgtcagct cgttagaaag atgattttga gaacctctga ggaaaccatt 300
tctacagttc aagaaaagca acaaaatatt tctcccctag tgagagaaag aggtcctcag 360
agagtagcgg atcctgtagc ccatgttgta gcaaaccctc aagctgaggg gcagctccag 420
tggctgaacc gccgggccaa tgccctcctg gccaatggcg tggagctgag agataaccag 480
ctggtggtgc catcagaggg cctgtacctc atctactccc aggtcctctt caagggccaa 540
ggctgccct ccacccatgt gctcctcacc cacaccatca gccgcatcgc cgtctcctac 600

RAW SEQUENCE LISTING DATE: 10/29/2004
PATENT APPLICATION: **US/10/006,305A** TIME: 13:08:30

Input Set : **A:\41673292.app**
Output Set: **N:\CRF4\10292004\J006305A.raw**

cagaccaagg tcaacctcct ctctgccatc aagagcccct gccagaggga gaccccagag 660
ggggctgagg ccaagccctg gtatgagccc atctatctgg gaggggtctt ccagctggag 720
aagggtgacc gactcagcgc tgagatcaat cggcccgact atctcgactt tgcggagtct 780
gggcaggtct actttggaat cattgctctg tga 813

<210> SEQ ID NO: 5
<211> LENGTH: 256
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa polypeptide encoded by the DNA sequence of SEQ ID NO:1
<400> SEQUENCE: 5

```
Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
 1               5                  10                  15
Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
            20                  25                  30
Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
        35                  40                  45
Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
    50                  55                  60
Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
65                  70                  75                  80
Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
                85                  90                  95
Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Asp Glu Asp Pro Val
            100                 105                 110
Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu
        115                 120                 125
Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp
    130                 135                 140
Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln
145                 150                 155                 160
Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr
                165                 170                 175
His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu
            180                 185                 190
Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala
        195                 200                 205
Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln
    210                 215                 220
Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr
225                 230                 235                 240
Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
                245                 250                 255
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<210> SEQ ID NO: 6
<211> LENGTH: 192
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

RAW SEQUENCE LISTING DATE: 10/29/2004
PATENT APPLICATION: **US/10/006,305A** TIME: 13:08:30

Input Set : **A:\41673292.app**
Output Set: **N:\CRF4\10292004\J006305A.raw**

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188 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TBFa
189       polypeptide encoded by the DNA sequence of SEQ ID NO:2
191 <400> SEQUENCE: 6
192 Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
193   1               5                  10                  15
195 Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile
196              20                  25                  30
198 Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Ala Asp Pro Val
199          35                  40                  45
201 Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu
202      50                  55                  60
204 Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp
205  65                  70                  75                  80
207 Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln
208                  85                  90                  95
210 Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr
211             100                 105                 110
213 His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu
214         115                 120                 125
216 Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala
217     130                 135                 140
219 Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln
220 145                 150                 155                 160
222 Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr
223                 165                 170                 175
225 Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
226             180                 185                 190
232 <210> SEQ ID NO: 7
233 <211> LENGTH: 278
234 <212> TYPE: PRT
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa
239       polypeptide encoded by the DNA sequence of SEQ ID NO:3
241 <400> SEQUENCE: 7
242 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
243   1               5                  10                  15
245 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
246              20                  25                  30
248 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
249          35                  40                  45
251 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
252      50                  55                  60
254 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
255  65                  70                  75                  80
257 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
258                  85                  90                  95
260 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
261             100                 105                 110
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PATENT APPLICATION: **US/10/006,305A** TIME: 13:08:30

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Output Set: **N:\CRF4\10292004\J006305A.raw**

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263 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
264         115                 120                 125
266 Lys Gln Ala Asp Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu
267     130                 135                 140
269 Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn
270 145                 150                 155                 160
272 Gly Val Glu Leu Arg Asp Asn Glu Leu Val Val Pro Ser Glu Gly Leu
273                 165                 170                 175
275 Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser
276             180                 185                 190
278 Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr
279         195                 200                 205
281 Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg
282     210                 215                 220
284 Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr
285 225                 230                 235                 240
287 Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu
288                 245                 250                 255
290 Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr
291             260                 265                 270
293 Phe Gly Ile Ile Ala Leu
294         275
297 <210> SEQ ID NO: 8
298 <211> LENGTH: 270
299 <212> TYPE: PRT
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa
304       polypeptide encoded by the DNA sequence of SEQ ID NO:4
306 <400> SEQUENCE: 8
307 Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
308   1               5                  10                  15
310 Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
311             20                  25                  30
313 Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
314         35                  40                  45
316 Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
317     50                  55                  60
319 Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
320 65                  70                  75                  80
322 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
323                 85                  90                  95
325 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
326             100                 105                 110
328 Leu Val Arg Glu Arg Glu Pro Gln Arg Val Ala Asp Pro Val Ala His
329         115                 120                 125
331 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
332     130                 135                 140
334 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
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VERIFICATION SUMMARY DATE: 10/29/2004
PATENT APPLICATION: **US/10/006,305A** TIME: 13:08:31

Input Set : **A:\41673292.app**
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